

## CLONING OF CYTOCHROME P450 GENES FROM NICOTIANA

The present invention relates to nucleic acid sequences encoding cytochrome p450 enzymes (hereinafter referred to as p450 and p450 enzymes) in *Nicotiana* plants and methods for using those nucleic acid sequences to alter plant phenotypes.

### BACKGROUND

Cytochrome p450s catalyze enzymatic reactions for a diverse range of chemically dissimilar substrates that include the oxidative, peroxidative and reductive metabolism of endogenous and xenobiotic substrates. In plants, p450s participate in biochemical pathways that include the synthesis of plant products such as phenylpropanoids, alkaloids, terpenoids, lipids, cyanogenic glycosides, and glucosinolates (Chappel, Annu. Rev. Plant Physiol. Plant Mol. Biol. 198, 49:311-343). Cytochrome p450s, also known as p450 heme-thiolate proteins, usually act as terminal oxidases in multi-component electron transfer chains, called p450-containing monooxygenase systems. Specific reactions catalyzed include demethylation, hydroxylation, epoxidation, N-oxidation, sulfoxidation, N-, S-, and O-dealkylations, desulfation, deamination, and reduction of azo, nitro, and N-oxide groups.

The diverse role of *Nicotiana* plant p450 enzymes has been implicated in effecting a variety of plant

metabolites such as phenylpropanoids, alkaloids, terpenoids, lipids, cyanogenic glycosides, glucosinolates and a host of other chemical entities. During recent years, it is becoming apparent that some p450 enzymes can impact the composition of plant metabolites in plants. For example, it has been long desired to improve the flavor and aroma of certain plants by altering its profile of selected fatty acids through breeding; however very little is known about mechanisms involved in controlling the levels of these leaf constituents. The down regulation of p450 enzymes associated with the modification of fatty acids may facilitate accumulation of desired fatty acids that provide more preferred leaf phenotypic qualities. The function of p450 enzymes and their broadening roles in plant constituents is still being discovered. For instance, a special class of p450 enzymes was found to catalyze the breakdown of fatty acid into volatile C6- and C9-aldehydes and -alcohols that are major contributors of "fresh green" odor of fruits and vegetables. The level of other novel targeted p450s may be altered to enhance the qualities of leaf constituents by modifying lipid composition and related break down metabolites in Nicotiana leaf. Several of these constituents in leaf are affected by senescence that stimulates the maturation of leaf quality properties. Still other reports have shown that p450s enzymes are play a functional role in altering fatty acids that are involved in plant-pathogen interactions and disease resistance.

In other instances, p450 enzymes have been suggested to be involved in alkaloid biosynthesis. Nornicotine is a minor alkaloid found in *Nicotiana tabaceum*. It has been postulated that it is produced by the p450 mediated demethylation of nicotine followed by acylation and nitrosation at the N position thereby producing a series of N-acylnonicotines and N-nitrosonornicotines. N-demethylation, catalyzed by a putative p450 demethylase, is thought to be a primary source of nornicotine biosyntheses in *Nicotiana*. While the enzyme is believed to be microsomal, thus far a nicotine demethylase enzyme has not been successfully purified, nor have the genes involved been isolated.

Furthermore, it is hypothesized but not proven that the activity of p450 enzymes is genetically controlled and also strongly influenced by environment factors. For example, the demethylation of nicotine in *Nicotiana* is thought to increase substantially when the plants reach a mature stage. Furthermore, it is hypothesized yet not proven that the demethylase gene contains a transposable element that can inhibit translation of RNA when present.

The large multiplicity of p450 enzyme forms, their differing structure and function have made their research on *Nicotiana* p450 enzymes very difficult before the enclosed invention. In addition, cloning of p450 enzymes has been hampered at least in part because these

membrane-localized proteins are typically present in low abundance and often unstable to purification. Hence, a need exists for the identification of p450 enzymes in plants and the nucleic acid sequences associated with those p450 enzymes. In particular, only a few cytochrome p450 proteins have been reported in *Nicotiana*. The inventions described herein entail the discovery of a substantial number of cytochrome p450 fragments that correspond to several groups of p450 species based on their sequence identity.

#### SUMMARY

The present invention is directed to plant p450 enzymes. The present invention is further directed to plant p450 enzymes from *Nicotiana*. The present invention is also directed to p450 enzymes in plants whose expression is induced by ethylene and/or plant senescence. The present invention is yet further directed to nucleic acid sequences in plants having enzymatic activities, for example, being categorized as oxygenase, demethylase and the like, or other and the use of those sequences to reduce or silence the expression or over-expression of these enzymes. The invention also relates to p450 enzymes found in plants containing higher nornicotine levels than plants exhibiting lower nornicotine levels.

In one aspect, the invention is directed to nucleic acid sequences as set forth in SEQ. ID. Nos. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,

37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63,  
65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91,  
95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117,  
119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139,  
143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163,  
165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185,  
187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,  
209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229,  
231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251,  
253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273,  
275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295 and  
297.

In a second related aspect, those fragments  
containing greater than 75% identity in nucleic acid  
sequence were placed into groups dependent upon their  
identity in a region corresponding to the first nucleic  
acid following the cytochrome p450 motif GXRXCX(G/A) to  
the stop codon. The representative nucleic acid groups  
and respective species are shown in Table I.

In a third aspect, the invention is directed to  
amino acid sequences as set forth in SEQ. ID. Nos. 2, 4,  
6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34,  
36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62,  
64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90,  
92, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116,  
118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138,  
140, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162,  
164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184,

186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206,  
208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228,  
230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250,  
252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272,  
274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294,  
296 and 298.

In a fourth related aspect, those fragments  
containing greater than 71% identity in amino acid  
sequence were placed into groups dependent upon their  
identity to each other in a region corresponding to the  
first amino acid following the cytochrome p450 motif  
GXRXCX(G/A) to the stop codon. The representative amino  
acid groups and respective species are shown in Table II.

In a fifth aspect, the invention is directed to  
amino acid sequences of full length genes as set forth in  
SEQ. ID. Nos. 150, 152, 154, 156, 158, 160, 162, 164,  
166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186,  
188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,  
210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230,  
232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252,  
254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274,  
276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296 and  
298.

In a sixth related aspect, those full length genes  
containing 85% or greater identity in amino acid sequence  
were placed into groups dependent upon the identity to

each other. The representative amino acid groups and respective species are shown in Table III.

5 In a seventh aspect, the invention is directed to amino acid sequences of the fragments set forth in SEQ. ID. Nos. 299-357.

10 In the eighth related aspect, those fragments containing 90% or greater identity in amino acid sequence were placed into groups dependent upon their identity to each other in a region corresponding to the first cytochrome p450 domain, UXXRXXZ, to the third cytochrome domain, GXR XO, where U is E or K, X is any amino acid and Z is R, T, S or M. The representative amino acid groups  
15 respective species shown in Table IV.

20 In a ninth related aspect, the reduction or elimination or over-expression of p450 enzymes in Nicotiana plants may be accomplished transiently using RNA viral systems.

25 Resulting transformed or infected plants are assessed for phenotypic changes including, but not limited to, analysis of endogenous p450 RNA transcripts, p450 expressed peptides, and concentrations of plant metabolites using techniques commonly available to one having ordinary skill in the art.

30 In a tenth important aspect, the present invention is also directed to generation of transgenic Nicotiana

lines that have altered p450 enzyme activity levels. In accordance with the invention, these transgenic lines include nucleic acid sequences that are effective for reducing or silencing or increasing the expression of certain enzyme thus resulting in phenotypic effects within Nicotiana. Such nucleic acid sequences include SEQ. ID. Nos. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295 and 297.

In a very important eleventh aspect of the invention, plant cultivars including nucleic acids of the present invention in a down regulation capacity using either full length genes or fragments thereof or in an over-expression capacity using full length genes will have altered metabolite profiles relative to control plants.

In a twelfth aspect of the invention, plant cultivars including nucleic acid of the present invention



using either full length genes or fragments thereof in  
modifying the biosynthesis or breakdown of metabolites  
derived from the plant or external to the plants, will  
have use in tolerating certain exogenous chemicals or  
plant pests. Such nucleic acid sequences include SEQ ID.  
Nos. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27,  
29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55,  
57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83,  
85, 87, 89, 91, 95, 97, 99, 101, 103, 105, 107, 109, 111,  
113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133,  
135, 137, 139, 143, 145, 147, 149, 151, 153, 155, 157,  
159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179,  
181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201,  
203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223,  
225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245,  
247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267,  
269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289,  
291, 293, 295 and 297.

In a thirteenth aspect, the present invention is  
directed to the screening of plants, more preferably  
Nicotiana, that contain genes that have substantial  
nucleic acid identity to the taught nucleic acid  
sequence. The use of the invention would be advantageous  
to identify and select plants that contain a nucleic acid  
sequence with exact or substantial identity where such  
plants are part of a breeding program for traditional or  
transgenic varieties, a mutagenesis program, or naturally  
occurring diverse plant populations. The screening of  
plants for substantial nucleic acid identity may be

accomplished by evaluating plant nucleic acid materials using a nucleic acid probe in conjunction with nucleic acid detection protocols including, but not limited to, nucleic acid hybridization and PCR analysis. The nucleic acid probe may consist of the taught nucleic acid sequence or fragment thereof corresponding to SEQ ID 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295 and 297.

In a fourteenth aspect, the present invention is directed to the identification of plant genes, more preferably Nicotiana, that share substantial amino acid identity corresponding to the taught nucleic acid sequence. The identification of plant genes including both cDNA and genomic clones, those cDNAs and genomic clones, more preferably from Nicotiana may be accomplished by screening plant cDNA libraries using a nucleic acid probe in conjunction with nucleic acid detection protocols including, but not limited to,

5 nucleic acid hybridization and PCR analysis. The nucleic acid probe may be comprised of nucleic acid sequence or fragment thereof corresponding to SEQ ID 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 143, 145 and 147.

10 In an alternative fifteenth aspect, cDNA expression libraries that express peptides may be screened using antibodies directed to part or all of the taught amino acid sequence. Such amino acid sequences include SEQ ID 15 2, 4, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 144, 146, 148.

20 In a sixteenth important aspect, the present invention is also directed to generation of transgenic Nicotiana lines that have over-expression of p450 enzyme activity levels. In accordance with the invention, these 25 transgenic lines include all nucleic acid sequences encoding the amino acid sequences of full length genes that are effective for increasing the expression of certain enzyme thus resulting in phenotypic effects 30 within Nicotiana. Such amino acid sequences include SEQ.

5 ID. 150, 152, 154, 156, 158, 160, 162, 164, 166, 168,  
170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,  
192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212,  
214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234,  
236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256,  
258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278,  
280, 282, 284, 286, 288, 290, 292, 294, 296 and 298.

#### BRIEF DESCRIPTION OF DRAWINGS

10 Figure 1 shows nucleic acid SEQ. ID. No.:1 and amino  
acid SEQ. ID. No.:2.

Figure 2 shows nucleic acid SEQ. ID. No.:3 and amino  
acid SEQ. ID. No.:4.

15 Figure 3 shows nucleic acid SEQ. ID. No.:5 and amino  
acid SEQ. ID. No.:6.

Figure 4 shows nucleic acid SEQ. ID. No.:7 and amino  
acid SEQ. ID. No.:8.

Figure 5 shows nucleic acid SEQ. ID. No.:9 and amino  
acid SEQ. ID. No.:10.

20 Figure 6 shows nucleic acid SEQ. ID. No.:11 and  
amino acid SEQ. ID. No.:12.

Figure 7 shows nucleic acid SEQ. ID. No.:13 and  
amino acid SEQ. ID. No.:14.

25 Figure 8 shows nucleic acid SEQ. ID. No.:15 and  
amino acid SEQ. ID. No.:16.

Figure 9 shows nucleic acid SEQ. ID. No.:17 and  
amino acid SEQ. ID. No.:18.

Figure 10 shows nucleic acid SEQ. ID. No.:19 and  
amino acid SEQ. ID. No.:20.

30 Figure 11 shows nucleic acid SEQ. ID. No.:21 and

amino acid SEQ. ID. No.:22.

Figure 12 shows nucleic acid SEQ. ID. No.:23 and amino acid SEQ. ID. No.:24.

Figure 13 shows nucleic acid SEQ. ID. No.:25 and amino acid SEQ. ID. No.:26.

Figure 14 shows nucleic acid SEQ. ID. No.:27 and amino acid SEQ. ID. No.:28.

Figure 15 shows nucleic acid SEQ. ID. No.:29 and amino acid SEQ. ID. No.:30.

Figure 16 shows nucleic acid SEQ. ID. No.:31 and amino acid SEQ. ID. No.:32.

Figure 17 shows nucleic acid SEQ. ID. No.:33 and amino acid SEQ. ID. No.:34.

Figure 18 shows nucleic acid SEQ. ID. No.:35 and amino acid SEQ. ID. No.:36.

Figure 19 shows nucleic acid SEQ. ID. No.:37 and amino acid SEQ. ID. No.:38.

Figure 20 shows nucleic acid SEQ. ID. No.:39 and amino acid SEQ. ID. No.:40.

Figure 21 shows nucleic acid SEQ. ID. No.:41 and amino acid SEQ. ID. No.:42.

Figure 22 shows nucleic acid SEQ. ID. No.:43 and amino acid SEQ. ID. No.:44.

Figure 23 shows nucleic acid SEQ. ID. No.:45 and amino acid SEQ. ID. No.:46.

Figure 24 shows nucleic acid SEQ. ID. No.:47 and amino acid SEQ. ID. No.:48.

Figure 25 shows nucleic acid SEQ. ID. No.:49 and amino acid SEQ. ID. No.:50.

Figure 26 shows nucleic acid SEQ. ID. No.:51 and

amino acid SEQ. ID. No.:52.

Figure 27 shows nucleic acid SEQ. ID. No.:53 and amino acid SEQ. ID. No.:54.

Figure 28 shows nucleic acid SEQ. ID. No.:55 and amino acid SEQ. ID. No.:56.

Figure 29 shows nucleic acid SEQ. ID. No.:57 and amino acid SEQ. ID. No.:58.

Figure 30 shows nucleic acid SEQ. ID. No.:59 and amino acid SEQ. ID. No.:60.

Figure 31 shows nucleic acid SEQ. ID. No.:61 and amino acid SEQ. ID. No.:62.

Figure 32 shows nucleic acid SEQ. ID. No.:63 and amino acid SEQ. ID. No.:64.

Figure 33 shows nucleic acid SEQ. ID. No.:65 and amino acid SEQ. ID. No.:66.

Figure 34 shows nucleic acid SEQ. ID. No.:67 and amino acid SEQ. ID. No.:68.

Figure 35 shows nucleic acid SEQ. ID. No.:69 and amino acid SEQ. ID. No.:70.

Figure 36 shows nucleic acid SEQ. ID. No.:71 and amino acid SEQ. ID. No.:72.

Figure 37 shows nucleic acid SEQ. ID. No.:73 and amino acid SEQ. ID. No.:74.

Figure 38 shows nucleic acid SEQ. ID. No.:75 and amino acid SEQ. ID. No.:76.

Figure 39 shows nucleic acid SEQ. ID. No.:77 and amino acid SEQ. ID. No.:78.

Figure 40 shows nucleic acid SEQ. ID. No.:79 and amino acid SEQ. ID. No.:80.

Figure 41 shows nucleic acid SEQ. ID. No.:81 and

amino acid SEQ. ID. No.:82.

Figure 42 shows nucleic acid SEQ. ID. No.:83 and amino acid SEQ. ID. No.:84.

Figure 43 shows nucleic acid SEQ. ID. No.:85 and amino acid SEQ. ID. No.:86.

Figure 44 shows nucleic acid SEQ. ID. No.:87 and amino acid SEQ. ID. No.:88.

Figure 45 shows nucleic acid SEQ. ID. No.:89 and amino acid SEQ. ID. No.:90.

Figure 46 shows nucleic acid SEQ. ID. No.:91 and amino acid SEQ. ID. No.:92.

Figure 48 shows nucleic acid SEQ. ID. No.:95 and amino acid SEQ. ID. No.:96.

Figure 49 shows nucleic acid SEQ. ID. No.:97 and amino acid SEQ. ID. No.:98.

Figure 50 shows nucleic acid SEQ. ID. No.:99 and amino acid SEQ. ID. No.:100.

Figure 51 shows nucleic acid SEQ. ID. No.:101 and amino acid SEQ. ID. No.:102.

Figure 52 shows nucleic acid SEQ. ID. No.:103 and amino acid SEQ. ID. No.:104.

Figure 53 shows nucleic acid SEQ. ID. No.:105 and amino acid SEQ. ID. No.:106.

Figure 54 shows nucleic acid SEQ. ID. No.:107 and amino acid SEQ. ID. No.:108.

Figure 55 shows nucleic acid SEQ. ID. No.:109 and amino acid SEQ. ID. No.:110.

Figure 56 shows nucleic acid SEQ. ID. No.:111 and amino acid SEQ. ID. No.:112.

Figure 57 shows nucleic acid SEQ. ID. No.:113 and

amino acid SEQ. ID. No.:114.

Figure 58 shows nucleic acid SEQ. ID. No.:115 and amino acid SEQ. ID. No.:116.

Figure 59 shows nucleic acid SEQ. ID. No.:117 and amino acid SEQ. ID. No.:118.

Figure 60 shows nucleic acid SEQ. ID. No.:119 and amino acid SEQ. ID. No.:120.

Figure 61 shows nucleic acid SEQ. ID. No.:121 and amino acid SEQ. ID. No.:122.

Figure 62 shows nucleic acid SEQ. ID. No.:123 and amino acid SEQ. ID. No.:124.

Figure 63 shows nucleic acid SEQ. ID. No.:125 and amino acid SEQ. ID. No.:126.

Figure 64 shows nucleic acid SEQ. ID. No.:127 and amino acid SEQ. ID. No.:128.

Figure 65 shows nucleic acid SEQ. ID. No.:129 and amino acid SEQ. ID. No.:130.

Figure 66 shows nucleic acid SEQ. ID. No.:131 and amino acid SEQ. ID. No.:132.

Figure 67 shows nucleic acid SEQ. ID. No.:133 and amino acid SEQ. ID. No.:134.

Figure 68 shows nucleic acid SEQ. ID. No.:135 and amino acid SEQ. ID. No.:136.

Figure 69 shows nucleic acid SEQ. ID. No.:137 and amino acid SEQ. ID. No.:138.

Figure 70 shows nucleic acid SEQ. ID. No.:139 and amino acid SEQ. ID. No.:140.

Figure 72 shows nucleic acid SEQ. ID. No.:143 and amino acid SEQ. ID. No.:144.

Figure 73 shows nucleic acid SEQ. ID. No.:145 and



amino acid SEQ. ID. No.:146.

Figure 74 shows nucleic acid SEQ. ID. No.:147 and amino acid SEQ. ID. No.:148.

Figure 75 shows nucleic acid SEQ. ID No.: 149 and amino acid SEQ. ID. No.: 150.

Figure 76 shows nucleic acid SEQ. ID No.: 151 and amino acid SEQ. ID. No.: 152.

Figure 77 shows nucleic acid SEQ. ID No.: 153 and amino acid SEQ. ID. No.: 154.

Figure 78 shows nucleic acid SEQ. ID No.: 155 and amino acid SEQ. ID. No.: 156.

Figure 79 shows nucleic acid SEQ. ID No.: 157 and amino acid SEQ. ID. No.: 158.

Figure 80 shows nucleic acid SEQ. ID No.: 159 and amino acid SEQ. ID. No.: 160.

Figure 81 shows nucleic acid SEQ. ID No.: 161 and amino acid SEQ. ID. No.: 162.

Figure 82 shows nucleic acid SEQ. ID No.: 163 and amino acid SEQ. ID. No.: 164.

Figure 83 shows nucleic acid SEQ. ID No.: 165 and amino acid SEQ. ID. No.: 166.

Figure 84 shows nucleic acid SEQ. ID No.: 167 and amino acid SEQ. ID. No.: 168.

Figure 85 shows nucleic acid SEQ. ID No.: 169 and amino acid SEQ. ID. No.: 170.

Figure 86 shows nucleic acid SEQ. ID No.: 171 and amino acid SEQ. ID. No.: 172.

Figure 87 shows nucleic acid SEQ. ID No.: 173 and amino acid SEQ. ID. No.: 174.

Figure 88 shows nucleic acid SEQ. ID No.: 175 and amino acid SEQ. ID. No.: 176.

Figure 89 shows nucleic acid SEQ. ID No.: 177 and amino acid SEQ. ID. No.: 178.

Figure 90 shows nucleic acid SEQ. ID No.: 179 and amino acid SEQ. ID. No.: 180.

Figure 91 shows nucleic acid SEQ. ID No.: 181 and amino acid SEQ. ID. No.: 182.

Figure 92 shows nucleic acid SEQ. ID No.: 183 and amino acid SEQ. ID. No.: 184.

Figure 93 shows nucleic acid SEQ. ID No.: 185 and amino acid SEQ. ID. No.: 186.

Figure 94 shows nucleic acid SEQ. ID No.: 187 and amino acid SEQ. ID. No.: 188.

Figure 95 shows nucleic acid SEQ. ID No.: 189 and amino acid SEQ. ID. No.: 190.

Figure 96 shows nucleic acid SEQ. ID No.: 191 and amino acid SEQ. ID. No.: 192.

Figure 97 shows nucleic acid SEQ. ID No.: 193 and amino acid SEQ. ID. No.: 194.

Figure 98 shows nucleic acid SEQ. ID No.: 195 and amino acid SEQ. ID. No.: 196.

Figure 99 shows nucleic acid SEQ. ID No.: 197 and amino acid SEQ. ID. No.: 198.

Figure 100 shows nucleic acid SEQ. ID No.: 199 and amino acid SEQ. ID. No.: 200.

Figure 101 shows nucleic acid SEQ. ID No.: 201 and amino acid SEQ. ID. No.: 202.

Figure 102 shows nucleic acid SEQ. ID No.: 203 and amino acid SEQ. ID. No.: 204.

Figure 103 shows nucleic acid SEQ. ID No.: 205 and amino acid SEQ. ID. No.: 206.

Figure 104 shows nucleic acid SEQ. ID No.: 207 and amino acid SEQ. ID. No.: 208.

5 Figure 105 shows nucleic acid SEQ. ID No.: 209 and amino acid SEQ. ID. No.: 210.

Figure 106 shows nucleic acid SEQ. ID No.: 211 and amino acid SEQ. ID. No.: 212.

10 Figure 107 shows nucleic acid SEQ. ID No.: 213 and amino acid SEQ. ID. No.: 214.

Figure 108 shows nucleic acid SEQ. ID No.: 215 and amino acid SEQ. ID. No.: 216.

Figure 109 shows nucleic acid SEQ. ID No.: 217 and amino acid SEQ. ID. No.: 218.

15 Figure 110 shows nucleic acid SEQ. ID No.: 219 and amino acid SEQ. ID. No.: 220.

Figure 111 shows nucleic acid SEQ. ID No.: 221 and amino acid SEQ. ID. No.: 222.

20 Figure 112 shows nucleic acid SEQ. ID No.: 223 and amino acid SEQ. ID. No.: 224.

Figure 113 shows nucleic acid SEQ. ID No.: 225 and amino acid SEQ. ID. No.: 226.

Figure 114 shows nucleic acid SEQ. ID No.: 227 and amino acid SEQ. ID. No.: 228.

25 Figure 115 shows nucleic acid SEQ. ID No.: 229 and amino acid SEQ. ID. No.: 230.

Figure 116 shows nucleic acid SEQ. ID No.: 231 and amino acid SEQ. ID. No.: 232.

30 Figure 117 shows nucleic acid SEQ. ID No.: 233 and amino acid SEQ. ID. No.: 234.

Figure 118 shows nucleic acid SEQ. ID No.: 235 and amino acid SEQ. ID. No.: 236.

Figure 119 shows nucleic acid SEQ. ID No.: 237 and amino acid SEQ. ID. No.: 238.

Figure 120 shows nucleic acid SEQ. ID No.: 239 and amino acid SEQ. ID. No.: 240.

Figure 121 shows nucleic acid SEQ. ID No.: 241 and amino acid SEQ. ID. No.: 242.

Figure 122 shows nucleic acid SEQ. ID No.: 243 and amino acid SEQ. ID. No.: 244.

Figure 123 shows nucleic acid SEQ. ID No.: 245 and amino acid SEQ. ID. No.: 246.

Figure 124 shows nucleic acid SEQ. ID No.: 247 and amino acid SEQ. ID. No.: 248.

Figure 125 shows nucleic acid SEQ. ID No.: 249 and amino acid SEQ. ID. No.: 250.

Figure 126 shows nucleic acid SEQ. ID No.: 251 and amino acid SEQ. ID. No.: 252.

Figure 127 shows nucleic acid SEQ. ID No.: 253 and amino acid SEQ. ID. No.: 254.

Figure 128 shows nucleic acid SEQ. ID No.: 255 and amino acid SEQ. ID. No.: 256.

Figure 129 shows nucleic acid SEQ. ID No.: 257 and amino acid SEQ. ID. No.: 258.

Figure 130 shows nucleic acid SEQ. ID No.: 259 and amino acid SEQ. ID. No.: 260.

Figure 131 shows nucleic acid SEQ. ID No.: 261 and amino acid SEQ. ID. No.: 262.

Figure 132 shows nucleic acid SEQ. ID No.: 263 and amino acid SEQ. ID. No.: 264.

Figure 133 shows nucleic acid SEQ. ID No.: 265 and  
amino acid SEQ. ID. No.: 266.

Figure 134 shows nucleic acid SEQ. ID No.: 267 and  
amino acid SEQ. ID. No.: 268.

5 Figure 135 shows nucleic acid SEQ. ID No.: 269 and  
amino acid SEQ. ID. No.: 270.

Figure 136 shows nucleic acid SEQ. ID No.: 271 and  
amino acid SEQ. ID. No.: 272.

10 Figure 137 shows nucleic acid SEQ. ID No.: 273 and  
amino acid SEQ. ID. No.: 274.

Figure 138 shows nucleic acid SEQ. ID No.: 275 and  
amino acid SEQ. ID. No.: 276.

Figure 139 shows nucleic acid SEQ. ID No.: 277 and  
amino acid SEQ. ID. No.: 278.

15 Figure 140 shows nucleic acid SEQ. ID No.: 279 and  
amino acid SEQ. ID. No.: 280.

Figure 141 shows nucleic acid SEQ. ID No.: 281 and  
amino acid SEQ. ID. No.: 282.

20 Figure 142 shows nucleic acid SEQ. ID No.: 283 and  
amino acid SEQ. ID. No.: 284.

Figure 143 shows nucleic acid SEQ. ID No.: 285 and  
amino acid SEQ. ID. No.: 286.

Figure 144 shows nucleic acid SEQ. ID No.: 287 and  
amino acid SEQ. ID. No.: 288.

25 Figure 145 shows nucleic acid SEQ. ID No.: 289 and  
amino acid SEQ. ID. No.: 290.

Figure 146 shows nucleic acid SEQ. ID No.: 291 and  
amino acid SEQ. ID. No.: 292.

30 Figure 147 shows nucleic acid SEQ. ID No.: 293 and  
amino acid SEQ. ID. No.: 294.

Figure 148 shows nucleic acid SEQ. ID No.: 295 and amino acid SEQ. ID. No.: 296.

Figure 149 shows nucleic acid SEQ. ID No.: 297 and amino acid SEQ. ID. No.: 298.

Figure 151 shows a comparison of Sequence Groups.

Figure 152 illustrates alignment of full length clones.

Figure 153 shows a procedure used for cloning of cytochrome p450 cDNA fragments by PCR

## DETAILED DESCRIPTION

### DEFINITIONS

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Singleton et al. (1994) Dictionary of Microbiology and Molecular Biology, second edition, John Wiley and Sons (New York) provides one of skill with a general dictionary of many of the terms used in this invention. All patents and publications referred to herein are incorporated by reference herein. For purposes of the present invention, the following terms are defined below.

"Enzymatic activity" is meant to include demethylation, hydroxylation, epoxidation, N-oxidation, sulfoxidation, N-, S-, and O- dealkylations, desulfation, deamination, and reduction of azo, nitro, and N-oxide groups. The term "nucleic acid" refers to a deoxyribonucleotide or ribonucleotide polymer in either

single- or double-stranded form, or sense or anti-sense,  
and unless otherwise limited, encompasses known analogues  
of natural nucleotides that hybridize to nucleic acids in  
a manner similar to naturally occurring nucleotides.  
Unless otherwise indicated, a particular nucleic acid  
sequence includes the complementary sequence thereof.

The terms "operably linked", "in operable  
combination", and "in operable order" refer to functional  
linkage between a nucleic acid expression control  
sequence (such as a promoter, signal sequence, or array  
of transcription factor binding sites) and a second  
nucleic acid sequence, wherein the expression control  
sequence affects transcription and/or translation of the  
nucleic acid corresponding to the second sequence.

The term "recombinant" when used with reference to  
a cell indicates that the cell replicates a heterologous  
nucleic acid, expresses said nucleic acid or expresses a  
peptide, heterologous peptide, or protein encoded by a  
heterologous nucleic acid. Recombinant cells can express  
genes or gene fragments in either the sense or antisense  
form that are not found within the native (non-  
recombinant) form of the cell. Recombinant cells can also  
express genes that are found in the native form of the  
cell, but wherein the genes are modified and re-  
introduced into the cell by artificial means.

A "structural gene" is that portion of a gene  
comprising a DNA segment encoding a protein, polypeptide  
or a portion thereof, and excluding the 5' sequence which

drives the initiation of transcription. The structural gene may alternatively encode a nontranslatable product. The structural gene may be one which is normally found in the cell or one which is not normally found in the cell or cellular location wherein it is introduced, in which case it is termed a "heterologous gene". A heterologous gene may be derived in whole or in part from any source known to the art, including a bacterial genome or episome, eukaryotic, nuclear or plasmid DNA, cDNA, viral DNA or chemically synthesized DNA. A structural gene may contain one or more modifications that could effect biological activity or its characteristics, the biological activity or the chemical structure of the expression product, the rate of expression or the manner of expression control. Such modifications include, but are not limited to, mutations, insertions, deletions and substitutions of one or more nucleotides. The structural gene may constitute an uninterrupted coding sequence or it may include one or more introns, bounded by the appropriate splice junctions. The structural gene may be translatable or non-translatable, including in an anti-sense orientation. The structural gene may be a composite of segments derived from a plurality of sources and from a plurality of gene sequences (naturally occurring or synthetic, where synthetic refers to DNA that is chemically synthesized).

"Derived from" is used to mean taken, obtained, received, traced, replicated or descended from a source (chemical and/or biological). A derivative may be



produced by chemical or biological manipulation (including, but not limited to, substitution, addition, insertion, deletion, extraction, isolation, mutation and replication) of the original source.

5 "Chemically synthesized", as related to a sequence of DNA, means that portions of the component nucleotides were assembled in vitro. Manual chemical synthesis of DNA may be accomplished using well established procedures (Caruthers, Methodology of DNA and RNA Sequencing, 10 (1983), Weissman (ed.), Praeger Publishers, New York, Chapter 1); automated chemical synthesis can be performed using one of a number of commercially available machines.

15 Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman and Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman Proc. Natl. Acad. Sci. (U.S.A.) 85: 20 2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by inspection.

25 The NCBI Basic Local Alignment Search Tool (BLAST) (Altschul et al., 1990) is available from several sources, including the National Center for Biological Information (NCBI, Bethesda, Md.) and on the Internet, 30 for use in connection with the sequence analysis programs

blastp, blastn, blastx, tblastn and tblastx. It can be  
accessed at <http://www.ncbi.nlm.nih.gov/BLAST/>. A  
description of how to determine sequence identity using  
this program is available at  
[http://www.ncbi.nlm.nih.gov/BLAST/blast\\_help.html](http://www.ncbi.nlm.nih.gov/BLAST/blast_help.html).

The terms "substantial amino acid identity" or  
"substantial amino acid sequence identity" as applied to  
amino acid sequences and as used herein denote a  
characteristic of a polypeptide, wherein the peptide  
comprises a sequence that has at least 70 percent  
sequence identity, preferably 80 percent amino acid  
sequence identity, more preferably 90 percent amino acid  
sequence identity, and most preferably at least 99 to 100  
percent sequence identity as compared to a reference  
group over region corresponding to the first amino acid  
following the cytochrome p450 motif GXRXCX(G/A) to the  
stop codon of the translated peptide.

The terms "substantial nucleic acid identity" or  
"substantial nucleic acid sequence identity" as applied  
to nucleic acid sequences and as used herein denote a  
characteristic of a polynucleotide sequence, wherein the  
polynucleotide comprises a sequence that has at least 75  
percent sequence identity, preferably 81 percent amino  
acid sequence identity, more preferably at least 91  
percent sequence identity, and most preferably at least  
99 to 100 percent sequence identity as compared to a  
reference group over region corresponding to the first

nucleic acid following the cytochrome p450 motif GXRXCX(G/A) to the stop codon of the translated peptide.

5 Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. Stringent conditions are sequence-dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C to about 20°C, 10 usually about 10°C to about 15°C, lower than the thermal melting point (T<sub>m</sub>) for the specific sequence at a defined ionic strength and pH. The T<sub>m</sub> is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a matched probe. Typically, 15 stringent conditions will be those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 60°C. For instance in a standard Southern hybridization procedure, stringent conditions will include an initial wash in 6xSSC at 42 °C 20 followed by one or more additional washes in 0.2xSSC at a temperature of at least about 55°C, typically about 60°C and often about 65°C.

25 Nucleotide sequences are also substantially identical for purposes of this invention when the polypeptides and/or proteins which they encode are substantially identical. Thus, where one nucleic acid sequence encodes essentially the same polypeptide as a second nucleic acid sequence, the two nucleic acid 30 sequences are substantially identical, even if they would

not hybridize under stringent conditions due to degeneracy permitted by the genetic code (see, Darnell et al. (1990) Molecular Cell Biology, Second Edition Scientific American Books W. H. Freeman and Company New York for an explanation of codon degeneracy and the genetic code). Protein purity or homogeneity can be indicated by a number of means well known in the art, such as polyacrylamide gel electrophoresis of a protein sample, followed by visualization upon staining. For certain purposes high resolution may be needed and HPLC or a similar means for purification may be utilized.

As used herein, the term "vector" is used in reference to nucleic acid molecules that transfer DNA segment(s) into a cell. A vector may act to replicate DNA and may reproduce independently in a host cell. The term "vehicle" is sometimes used interchangeably with "vector." The term "expression vector" as used herein refers to a recombinant DNA molecule containing a desired coding sequence and appropriate nucleic acid sequences necessary for the expression of the operably linked coding sequence in a particular host organism. Nucleic acid sequences necessary for expression in prokaryotes usually include a promoter, an operator (optional), and a ribosome binding site, often along with other sequences. Eucaryotic cells are known to utilize promoters, enhancers, and termination and polyadenylation signals.

For the purpose of regenerating complete genetically engineered plants with roots, a nucleic acid may be inserted into plant cells, for example, by any technique such as in vivo inoculation or by any of the known in vitro tissue culture techniques to produce transformed plant cells that can be regenerated into complete plants. Thus, for example, the insertion into plant cells may be by in vitro inoculation by pathogenic or non-pathogenic *A. tumefaciens*. Other such tissue culture techniques may also be employed.

"Plant tissue" includes differentiated and undifferentiated tissues of plants, including, but not limited to, roots, shoots, leaves, pollen, seeds, tumor tissue and various forms of cells in culture, such as single cells, protoplasts, embryos and callus tissue. The plant tissue may be in planta or in organ, tissue or cell culture.

"Plant cell" as used herein includes plant cells in planta and plant cells and protoplasts in culture.

"cDNA" or "complementary DNA" generally refers to a single stranded DNA molecule with a nucleotide sequence that is complementary to an RNA molecule. cDNA is formed by the action of the enzyme reverse transcriptase on an RNA template.

#### STRATEGIES FOR OBTAINING NUCLEIC ACID SEQUENCES

5 In accordance with the present invention, RNA was extracted from Nicotiana tissue of converter and non-converter Nicotiana lines. The extracted RNA was then used to create cDNA. Nucleic acid sequences of the present invention were then generated using two strategies.

10 In the first strategy, the poly A enriched RNA was extracted from plant tissue and cDNA was made by reverse transcription PCR. The single strand cDNA was then used to create p450 specific PCR populations using degenerate primers plus a oligo d(T) reverse primer. The primer design was based on the highly conserved motifs of p450. Examples of specific degenerate primers are set forth in  
15 Figure 1. Sequence fragments from plasmids containing appropriate size inserts were further analyzed. These size inserts typically ranged from about 300 to about 800 nucleotides depending on which primers were used.

20 In a second strategy, a cDNA library was initially constructed. The cDNA in the plasmids was used to create p450 specific PCR populations using degenerate primers plus T7 primer on plasmid as reverse primer. As in the first strategy, sequence fragments from plasmids  
25 containing appropriate size inserts were further analyzed.

Nicotiana plant lines known to produce high levels of nornicotine (converter) and plant lines having

undetectable levels of nornicotine may be used as starting materials.

5 Leaves can then be removed from plants and treated with ethylene to activate p450 enzymatic activities defined herein. Total RNA is extracted using techniques known in the art. cDNA fragments can then be generated using PCR (RT-PCR) with the oligo d(T) primer as described in Figure 153. The cDNA library can then be  
10 constructed more fully described in examples herein.

15 The conserved region of p450 type enzymes can be used as a template for degenerate primers (Figure 75). Using degenerate primers, p450 specific bands can be amplified by PCR. Bands indicative for p450 like enzymes can be identified by DNA sequencing. PCR fragments can be characterized using BLAST search, alignment or other  
20 tools to identify appropriate candidates.

25 Sequence information from identified fragments can be used to develop PCR primers. These primers in combination of plasmid primers in cDNA library were used to clone full length p450 genes. Large-scale Southern reverse analysis was conducted to examine the differential expression for all fragment clones obtained and in some cases full length clones. In this aspect of the invention, these large-scale reverse Southern assays can be conducted using labeled total cDNA's from

different tissues as a probe to hybridize with cloned DNA fragments in order to screen all cloned inserts.

5 Nonradioactive and radioactive ( $P^{32}$ ) Northern blotting assays were also used to characterize clones p450 fragments and full length clones.

10 Peptide specific antibodies were made against several full-length clones by deriving their amino acid sequence and selecting peptide regions that were antigenic and unique relative to other clones. Rabbit antibodies were made to synthetic peptides conjugated to a carrier protein. Western blotting analyses or other immunological methods were performed on plant tissue  
15 using these antibodies.

20 Nucleic acid sequences identified as described above can be examined by using virus induced gene silencing technology (VIGS, Baulcombe, Current Opinions in Plant Biology, 1999, 2:109-113).

25 Peptide specific antibodies were made for several full-length clones by deriving their amino acid sequence and selecting peptide regions that were potentially antigenic and were unique relative to other clones. Rabbit antibodies were made to synthetic peptides conjugated to a carrier protein. Western blotting analyses were performed using these antibodies.



5 In another aspect of the invention, interfering RNA  
technology (RNAi) is used to further characterize  
cytochrome p450 enzymatic activities in Nicotiana plants  
of the present invention. The following references which  
describe this technology are incorporated by reference  
herein, Smith et al., Nature, 2000, 407:319-320; Fire et  
al., Nature, 1998, 391:306- 311; Waterhouse et al., PNAS,  
1998, 95:13959-13964; Stalberg et al., Plant Molecular  
Biology, 1993, 23:671- 683; Baulcombe, Current Opinions  
10 in Plant Biology, 1999, 2:109-113; and Brigneti et al.,  
EMBO Journal, 1998, 17(22):6739-6746. Plants may be  
transformed using RNAi techniques, antisense techniques,  
or a variety of other methods described.

15 Several techniques exist for introducing foreign  
genetic material into plant cells, and for obtaining  
plants that stably maintain and express the introduced  
gene. Such techniques include acceleration of genetic  
material coated onto microparticles directly into cells  
20 (US Patents 4,945,050 to Cornell and 5,141,131 to  
DowElanco). Plants may be transformed using  
Agrobacterium technology, see US Patent 5,177,010 to  
University of Toledo, 5,104,310 to Texas A&M, European  
Patent Application 0131624B1, European Patent  
25 Applications 120516, 159418B1, European Patent  
Applications 120516, 159418B1 and 176,112 to Schilperoot,  
US Patents 5,149,645, 5,469,976, 5,464,763 and 4,940,838  
and 4,693,976 to Schilperoot, European Patent  
Applications 116718, 290799, 320500 all to MaxPlanck,  
30 European Patent Applications 604662 and 627752 to Japan

5 Nicotiana, European Patent Applications 0267159, and  
0292435 and US Patent 5,231,019 all to Ciba Geigy, US  
Patents 5,463,174 and 4,762,785 both to Calgene, and US  
Patents 5,004,863 and 5,159,135 both to Agracetus. Other  
transformation technology includes whiskers technology,  
see U.S. Patents 5,302,523 and 5,464,765 both to Zeneca.  
Electroporation technology has also been used to  
transform plants, see WO 87/06614 to Boyce Thompson  
Institute, 5,472,869 and 5,384,253 both to Dekalb,  
10 WO9209696 and WO9321335 both to PGS. All of these  
transformation patents and publications are incorporated  
by reference. In addition to numerous technologies for  
transforming plants, the type of tissue which is  
contacted with the foreign genes may vary as well. Such  
15 tissue would include but would not be limited to  
embryogenic tissue, callus tissue type I and II,  
hypocotyl, meristem, and the like. Almost all plant  
tissues may be transformed during dedifferentiation using  
appropriate techniques within the skill of an artisan.

20 Foreign genetic material introduced into a plant may  
include a selectable marker. The preference for a  
particular marker is at the discretion of the artisan,  
but any of the following selectable markers may be used  
25 along with any other gene not listed herein which could  
function as a selectable marker. Such selectable markers  
include but are not limited to aminoglycoside  
phosphotransferase gene of transposon Tn5 (Aph II) which  
encodes resistance to the antibiotics kanamycin, neomycin  
30 and G418, as well as those genes which code for

resistance or tolerance to glyphosate; hygromycin; methotrexate; phosphinothricin (bar); imidazolinones, sulfonylureas and triazolopyrimidine herbicides, such as chlorosulfuron; bromoxynil, dalapon and the like.

5 In addition to a selectable marker, it may be desirous to use a reporter gene. In some instances a reporter gene may be used without a selectable marker. Reporter genes are genes which are typically not present  
10 or expressed in the recipient organism or tissue. The reporter gene typically encodes for a protein which provide for some phenotypic change or enzymatic property. Examples of such genes are provided in K. Weising et al. Ann. Rev. Genetics, 22, 421 (1988), which is incorporated  
15 herein by reference. Preferred reporter genes include without limitation glucuronidase (GUS) gene and GFP genes.

20 Once introduced into the plant tissue, the expression of the structural gene may be assayed by any means known to the art, and expression may be measured as mRNA transcribed, protein synthesized, or the amount of gene silencing that occurs (see U.S. Patent No. 5,583,021 which is hereby incorporated by reference).  
25 Techniques are known for the in vitro culture of plant tissue, and in a number of cases, for regeneration into whole plants (EP Appln No. 88810309.0). Procedures for transferring the introduced expression complex to commercially useful cultivars are known to those skilled  
30 in the art.

5           Once plant cells expressing the desired level of p450 enzyme are obtained, plant tissues and whole plants can be regenerated therefrom using methods and techniques well-known in the art. The regenerated plants are then reproduced by conventional means and the introduced genes can be transferred to other strains and cultivars by conventional plant breeding techniques.

10           The following examples illustrate methods for carrying out the invention and should be understood to be illustrative of, but not limiting upon, the scope of the invention which is defined in the appended claims.

#### EXAMPLES

15           EXAMPLE I: DEVELOPMENT OF PLANT TISSUE AND ETHYLENE TREATMENT

20           Plant Growth

25           Plants were seeded in pots and grown in a greenhouse for 4 weeks. The 4 week old seedlings were transplanted into individual pots and grown in the greenhouse for 2 months. The plants were watered 2 times a day with water containing 150ppm NPK fertilizer during growth. The expanded green leaves were detached from plants to do the ethylene treatment described below.

30           Cell Line 78379

5 Tobacco line 78379, which is a burley tobacco line released by the University of Kentucky was used as a source of plant material. One hundred plants were cultured as standard in the art of growing tobacco and transplanted and tagged with a distinctive number (1-100). Fertilization and field management were conducted as recommended.

10 Three quarters of the 100 plants converted between 20 and 100% of the nicotine to nornicotine. One quarter of the 100 plants converted less than 5% of the nicotine to nornicotine. Plant number 87 had the least conversion (2%) while plant number 21 had 100% conversion. Plants  
15 converting less than 3% were classified as non-converters. Self-pollinated seed of plant number 87 and plant number 21, as well as crossed (21 x 87 and 87 x 21) seeds were made to study genetic and phenotypic differences. Plants from selfed 21 were converters, and  
20 99% of selfs from 87 were non-converters. The other 1% of the plants from 87 showed low conversion (5-15%). Plants from reciprocal crosses were all converters.

### Cell Line 4407

Nicotiana line 4407, which is a burley line was used as a source of plant material. Uniform and representative plants (100) were selected and tagged. Of the 100 plants 97 were non-converters and three were converters. Plant number 56 had the least amount of conversion (1.2%) and plant number 58 had the highest level of conversion (96%). Self-pollenated seeds and crossed seeds were made with these two plants.

Plants from selfed-58 segregated with 3:1 converter to non-converter ratio. Plants 58-33 and 58-25, were identified as homozygous converter and nonconverter plant lines, respectively. The stable conversion of 58-33 was confirmed by analysis of its progenies of next generation.

### Cell Line PBLB01

PBLB01 is a burley line developed by ProfiGen, Inc. and was used as a source of plant material. The converter plant was selected from foundation seeds of PBLB01.

### Ethylene Treatment Procedures

Green leaves were detached from 2-3 month greenhouse grown plants and sprayed with 0.3% ethylene solution (Prep brand Ethephon (Rhone-Poulenc)). Each sprayed leaf

was hung in a curing rack equipped with humidifier and covered with plastic. During the treatment, the sample leaves were periodically sprayed with the ethylene solution. Approximately 24-48 hour post ethylene treatment, leaves were collected for RNA extraction. Another sub-sample was taken for metabolic constituent analysis to determine the concentration of leaf metabolites and more specific constituents of interest such as a variety of alkaloids.

As an example, alkaloids analysis could be performed as follows. Samples (0.1 g) were shaken at 150 rpm with 0.5 ml 2N NaOH, and a 5 ml extraction solution which contained quinoline as an internal standard and methyl t-butyl ether. Samples were analyzed on a HP 6890 GC equipped with a FID detector. A temperature of 250°C was used for the detector and injector. An HP column (30m-0.32mm-1m) consisting of fused silica crosslinked with 5% phenol and 95% methyl silicon was used at a temperature gradient of 110-185 °C at 10°C per minute. The column was operated at 100°C with a flow rate of 1.7cm<sup>3</sup>min<sup>-1</sup> with a split ratio of 40:1 with a 2:1 injection volume using helium as the carrier gas.

#### EXAMPLE 2: RNA ISOLATION

For RNA extractions, middle leaves from 2 month old greenhouse grown plants were treated with ethylene as described. The 0 and 24-48 hours samples were used for RNA extraction. In some cases, leaf samples under the

senescence process were taken from the plants 10 days post flower-head removal. These samples were also used for extraction. Total RNA was isolated using Rneasy Plant Mini Kit® (Qiagen, Inc., Valencia, California) following manufacturer's protocol.

The tissue sample was ground under liquid nitrogen to a fine powder using a DEPC treated mortar and pestle. Approximately 100 milligrams of ground tissue were transferred to a sterile 1.5 ml eppendorf tube. This sample tube was placed in liquid nitrogen until all samples were collected. Then, 450µl of Buffer RLT as provided in the kit (with the addition of Mercaptoethanol) was added to each individual tube. The sample was vortexed vigorously and incubated at 56° C for 3 minutes. The lysate was then, applied to the QIAshredder™ spin column sitting in a 2-ml collection tube, and centrifuged for 2 minutes at maximum speed. The flow through was collected and 0.5 volume of ethanol was added to the cleared lysate. The sample is mixed well and transferred to an Rneasy® mini spin column sitting in a 2 ml collection tube. The sample was centrifuged for 1 minute at 10,000rpm. Next, 700µl of buffer RW1 was pipetted onto the Rneasy® column and centrifuged for 1 minute at 10,000rpm. Buffer RPE was pipetted onto the Rneasy® column in a new collection tube and centrifuged for 1 minute at 10,000 rpm. Buffer RPE was again, added to the Rneasy® spin column and



centrifuged for 2 minutes at maximum speed to dry the membrane. To eliminate any ethanol carry over, the membrane was placed in a separate collection tube and centrifuged for an additional 1 minute at maximum speed. The Rneasy® column was transferred into a new 1.5 ml collection tube, and 40 µl of Rnase-free water was pipetted directly onto the Rneasy® membrane. This final elute tube was centrifuged for 1 minute at 10,000rpm. Quality and quantity of total RNA was analyzed by denatured formaldehyde gel and spectrophotometer.

Poly(A)RNA was isolated using Oligotex™ poly A+ RNA purification kit (Qiagen Inc.) following manufacture's protocol. About 200 µg total RNA in 250 µl maximum volume was used. A volume of 250µl of Buffer OBB and 15 µl of Oligotex™ suspension was added to the 250 µl of total RNA. The contents were mixed thoroughly by pipetting and incubated for 3 minutes at 70°C on a heating block. The sample was then, placed at room temperature for approximately 20 minutes. The oligotex:mRNA complex was pelleted by centrifugation for 2 minutes at maximum speed. All but 50 µl of the supernatant was removed from the microcentrifuge tube. The sample was treated further by OBB buffer. The oligotex:mRNA pellet was resuspended in 400 µl of Buffer OW2 by vortexing. This mix was transferred onto a small spin column placed in a new tube and centrifuged for 1 minute at maximum speed. The spin column was transferred to a new tube and an additional 400 µl of Buffer OW2 was

5 added to the column. The tube was then centrifuged for 1 minute at maximum speed. The spin column was transferred to a final 1.5ml microcentrifuge tube. The sample was eluted with 60 ul of hot (70°C) Buffer OEB. Poly A product was analyzed by denatured formaldehyde gels and spectrophotometric analysis.

### EXAMPLE 3: REVERSE TRANSCRIPTION-PCR

10 First strand cDNA was produced using SuperScript reverse transcriptase following manufacturer's protocol (Invitrogen, Carlsbad, California). The poly A+ enriched RNA/oligo dT primer mix consisted of less than 5 µg of total RNA, 1 µl of 10mM dNTP mix, 1 µl of Oligo d(T)<sub>12-18</sub> (0.5µg/µl), and up to 10 µl of DEPC-treated  
15 water. Each sample was incubated at 65°C for 5 minutes, then placed on ice for at least 1 minute. A reaction mixture was prepared by adding each of the following components in order: 2 µl 10X RT buffer, 4  
20 µl of 25 mM MgCl<sub>2</sub>, 2µl of 0.1 M DTT, and 1 µl of RNase OUT Recombinant RNase Inhibitor. An addition of 9 µl of reaction mixture was pipetted to each RNA/primer mixture and gently mixed. It was incubated at 42°C for 2 minutes and 1 µl of Super Script II™ RT was added to  
25 each tube. The tube was incubated for 50 minutes at 42°C. The reaction was terminated at 70°C for 15 minutes and chilled on ice. The sample was collected by centrifugation and 1 µl of RNase H was added to each tube and incubated for 20 minutes at 37°C. The second  
30 PCR was carried out with 200 pmoles of forward primer

(degenerate primers as in Figure 75, SEQ.ID Nos. 149-156) and 100 pmoles reverse primer (mix of 18nt oligo d(T) followed by 1 random base).

5           Reaction conditions were 94°C for 2 minutes and then performed 40 cycles of PCR at 94°C for 1 minute, 45' to 60°C for 2 minutes, 72°C for 3 minutes with a 72°C extension for an extra 10 min.

10           Ten microliters of the amplified sample were analyzed by electrophoresis using a 1% agarose gel. The correct size fragments were purified from agarose gel.

15           EXAMPLE 4: GENERATION OF PCR FRAGMENT POPULATIONS

20           PCR fragments from Example 3 were ligated into a pGEM-T® Easy Vector (Promega, Madison, Wisconsin) following manufacturer's instructions. The ligated product was transformed into JM109 competent cells and plated on LB media plates for blue/white selection. Colonies were selected and grown in a 96 well plate with 1.2 ml of LB media overnight at 37°C. Frozen stock was generated for all selected colonies. Plasmid DNA from plates were purified using Beckman's Biomeck 25           2000 miniprep robotics with Wizard SV Miniprep® kit (Promega). Plasmid DNA was eluted with 100µl water and stored in a 96 well plate. Plasmids were digested by

EcoR1 and were analyzed using 1% agarose gel to confirm the DNA quantity and size of inserts. The plasmids containing a 400-600 bp insert were sequenced using an CEQ 2000 sequencer (Beckman, Fullerton, California). The sequences were aligned with GenBank database by BLAST search. The p450 related fragments were identified and further analyzed. Alternatively, p450 fragments were isolated from subtraction libraries. These fragments were also analyzed as described above.

#### EXAMPLE 5: CONSTRUCTION OF CDNA LIBRARY

A cDNA library was constructed by preparing total RNA from ethylene treated leaves as follows. First, total RNA was extracted from ethylene treated leaves of tobacco line 58-33 using a modified acid phenol and chloroform extraction protocol. Protocol was modified to use one gram of tissue that was ground and subsequently vortexed in 5 ml of extraction buffer (100 mM Tris-HCl, pH 8.5; 200 mM NaCl; 10mM EDTA; 0.5% SDS) to which 5 ml phenol (pH5.5) and 5 ml chloroform was added. The extracted sample was centrifuged and the supernatant was saved. This extraction step was repeated 2-3 more times until the supernatant appeared clear. Approximately 5 ml of chloroform was added to remove trace amounts of phenol. RNA was precipitated from the combined supernatant fractions by adding a 3-fold volume of ETOH and 1/10 volume of 3M NaOAc (pH5.2) and storing at -20°C for 1 hour. After transferring to

a Corex glass container the RNA fraction was centrifuged at 9,000 RPM for 45 minutes at 4°C. The pellet was washed with 70% ethanol and spun for 5 minutes at 9,000 RPM at 4°C. After drying the pellet, the pelleted RNA was dissolved in 0.5 ml RNase free water. The pelleted RNA was dissolved in 0.5 ml RNase free water. The quality and quantity of total RNA was analyzed by denatured formaldehyde gel and spectrophotometer, respectively.

The resultant total RNA was isolated for poly A+ RNA using an Oligo(dT) cellulose protocol (Invitrogen) and Microcentrifuge spin columns (Invitrogen) by the following protocol. Approximately twenty mg of total RNA was subjected to twice purification to obtain high quality poly A+ RNA. Poly A+ RNA product was analyzed by performing denatured formaldehyde gel and subsequent RT-PCR of known full-length genes to ensure high quality of mRNA.

Next, poly A+ RNA was used as template to produce a cDNA library employing cDNA synthesis kit, ZAP-cDNA® synthesis kit, and ZAP-cDNA® Gigapack® III gold cloning kit (Stratagene, La Jolla, California). The method involved following the manufacture's protocol as specified. Approximately 8 µg of poly A+ RNA was used to construct cDNA library. Analysis of the primary library revealed about  $2.5 \times 10^6$  -  $1 \times 10^7$  pfu. A quality background test of the library was completed by

complementation assays using IPTG and X-gal, where recombinant plaques was expressed at more than 100-fold above the background reaction.

5           A more quantitative analysis of the library by random PCR showed that average size of insert cDNA was approximately 1.2 kb. The method used a two-step PCR method as followed. For the first step, reverse  
10           primers were designed based on the preliminary sequence information obtained from p450 fragments. The designed reverse primers and T3 (forward) primers were used  
          amplify corresponding genes from the cDNA library. PCR reactions were subjected to agarose electrophoresis and  
15           the corresponding bands of high molecular weight were excised, purified, cloned and sequenced. In the second  
          step, new primers designed from 5'UTR or the start coding region of p450 as the forward primers together  
          with the reverse primers (designed from 3'UTR of p450) were used in the subsequent PCR to obtain full-length  
20           p450 clones.

          The p450 fragments were generated by PCR amplification from the constructed cDNA library as  
25           described in Example 3 with the exception of the reverse primer. The T7 primer located on the plasmid  
          downstream of cDNA inserts (see Figure 75) was used as a reverse primer. PCR fragments were isolated, cloned  
          and sequenced as described in Example 4.

30           Full-length p450 genes were isolated by PCR method

from constructed cDNA library. Gene specific reverse primers (designed from the downstream sequence of p450 fragments) and a forward primer (T3 on library plasmid) were used to clone the full length genes. PCR fragments were isolated, cloned and sequenced. If necessary, second step PCR was applied. In the second step, new forward primers designed from 5'UTR of cloned p450s together with the reverse primers designed from 3'UTR of p450 clones were used in the subsequent PCR reactions to obtain full-length p450 clones. The clones were subsequently sequenced.

#### EXAMPLE 6: CHARACTERIZATION OF CLONED FRAGMENTS - REVERSE SOUTHERN BLOTTING ANALYSIS

Nonradioactive large scale reverse southern blotting assays were performed on all p450 clones identified in above examples to detect the differential expression. It was observed that the level of expression among different p450 clusters was very different. Further real time detection was conducted on those with high expression.

Nonradioactive Southern blotting procedures were conducted as follows.

1) Total RNA was extracted from ethylene treated and nontreated converter (58-33) and nonconverter (58-25) leaves using the Qiagen Rnaeasy kit as described in Example 2.

2) Probe was produced by biotin-tail labeling a single strand cDNA derived from poly A+ enriched RNA generated in above step. This labeled single strand cDNA was generated by RT-PCR of the converter and nonconverter total RNA (Invitrogen) as described in Example 3 with the exception of using biotinylated oligo dT as a primer (Promega). These were used as a probe to hybridize with cloned DNA.

3) Plasmid DNA was digested with restriction enzyme EcoR1 and run on agarose gels. Gels were simultaneously dried and transferred to two nylon membranes (Biodyne B®). One membrane was hybridized with converter probe and the other with nonconverter probe. Membranes were UV-crosslinked (auto crosslink setting, 254 nm, Stratagene, Stratalinker) before hybridization.

Alternatively, the inserts were PCR amplified from each plasmid using the sequences located on both arms of p-GEM plasmid, T3 and SP6, as primers. The PCR products were analyzed by running on a 96 well Ready-to-run agarose gels. The confirmed inserts were dotted on two nylon membranes. One membrane was hybridized with converter probe and the other with nonconverter probe.

4) The membranes were hybridized and washed following manufacture's instruction with the



modification of washing stringency (Enzo MaxSence™ kit,  
Enzo Diagnostics, Inc, Farmingdale, NY). The membranes  
were prehybridized with hybridization buffer (2x SSC  
buffered formamide, containing detergent and  
hybridization enhancers) at 42°C for 30 min and  
hybridized with 10μl denatured probe overnight at 42°C.  
The membranes then were washed in 1X hybridization wash  
buffer 1 time at room temperature for 10 min and 4  
times at 68°C for 15 min. The membranes were ready for  
the detection.

5) The washed membranes were detected by alkaline  
phosphatase labeling followed by NBT/BCIP colometric  
detection as described in manufacture's detection  
procedure (Enzo Diagnostics, Inc.). The membranes were  
blocked for one hour at room temperature with 1x  
blocking solution, washed 3 times with 1X detection  
reagents for 10 min, washed 2 times with 1x  
predevelopment reaction buffer for 5 min and then  
developed the blots in developing solution for 30-45  
min until the dots appear. All reagents were provided  
by manufacture (Enzo Diagnostics, Inc). In Addition,  
large scale reverse Southern assay was also performed  
using KPL southern hybridization and detection kit™  
following manufacturer's instruction (KPL, Gaithersburg,  
Maryland).

# EXAMPLE 7: CHARACTERIZATION OF CLONES - NORTHERN BLOT ANALYSIS

Alternative to Southern Blot analysis, some  
5 membranes were hybridized and detected as described in  
the example of Northern blotting assays. Northern  
Hybridization was used to detect mRNA differentially  
expressed in Nicotiana as follows.

10 A random priming method was used to prepare probes  
from cloned p450 (Megaprime™ DNA Labelling Systems,  
Amersham Biosciences).

15 The following components were mixed: 25ng  
denatured DNA template; 4ul of each unlabeled dTTP,  
dGTP and dCTP; 5ul of reaction buffer; P<sup>32</sup>-labelled  
dATP and 2ul of Klenow I; and H<sub>2</sub>O, to bring the  
reaction to 50ul. The mixture was incubated in 37°C  
for 1-4 hours, then stopped with 2ul of 0.5 M EDTA.  
20 The probe was denatured by incubating at 95°C for 5  
minutes before use.

25 RNA samples were prepared from ethylene treated  
and non-treated fresh leaves of several pairs of  
tobacco lines. In some cases poly A+ enriched RNA was  
used. Approximately 15µg total RNA or 1.8µg mRNA  
(methods of RNA and mRNA extraction as described in  
Example 5) were brought to equal volume with DEPC H<sub>2</sub>O  
(5-10 µl). The same volume of loading buffer (1 x  
30 MOPS; 18.5 % Formaldehyde; 50 % Formamide; 4 %

Ficoll400; Bromophenolblue) and 0.5  $\mu$ l EtBr (0.5  $\mu$ g/ $\mu$ l) were added. The samples were subsequently denatured in preparation for separation of the RNA by electrophoresis.

Samples were subjected to electrophoresis on a formaldehyde gel (1 % Agarose, 1 x MOPS, 0.6 M Formaldehyde) with 1XMOP buffer (0.4 M Morpholinopropanesulfonic acid; 0.1 M Na-acetate-3 x H<sub>2</sub>O; 10 mM EDTA; adjust to pH 7.2 with NaOH). RNA was transferred to a Hybond-N+ membrane (Nylon, Amersham Pharmacia Biotech) by capillary method in 10 X SSC buffer (1.5 M NaCl; 0.15 M Na-citrate) for 24 hours. Membranes with RNA samples were UV-crosslinked (auto crosslink setting, 254 nm, Stratagene, Stratalinker) before hybridization.

The membrane was prehybridized for 1-4 hours at 42°C with 5-10 ml prehybridization buffer (5 x SSC; 50 % Formamide; 5 x Denhardt's-solution; 1 % SDS; 100 $\mu$ g/ml heat-denatured sheared non- homologous DNA). Old prehybridization buffer was discarded, and new prehybridization buffer and probe were added. The hybridization was carried out over night at 42°C. The membrane was washed for 15 minutes with 2 x SSC at room temperature, followed by a wash with 2 x SSC.

A major focus of the invention was the discovery of novel genes that may be induced as a result of ethylene treatment or play a key role in tobacco leaf quality and constituents. As illustrated in the table below, Northern blots and reverse Southern Blot were useful in determining which genes were induced by ethylene treatment relative to non-induced plants. Interestingly, not all fragments were affected similarly in the converter and nonconverter. The cytochrome p450 fragments of interest were partially sequenced to determine their structural relatedness. This information was used to subsequently isolate and characterize full length gene clones of interest.

Fragments	Induced mRNA Expression Ethylene Treatment
	Converter
D56-AC7 (SEQ ID No: 35)	+
D56-AG11 (SEQ ID No: 31)	+
D56-AC12 (SEQ ID No: 45)	+
D70A-AB5 (SEQ ID No: 95)	+
D73-AC9 (SEQ ID No: 43)	+
D70A-AA12 (SEQ ID No: 131)	+
D73A-AG3 (SEQ ID No: 129)	+
D34-52 (SEQ ID No: 61)	+
D56-AG6 (SEQ ID No: 51)	+

Northern analysis was performed using full length clones on tobacco tissue obtained from converter and nonconverter burley lines that were induced by ethylene treatment. The purpose was to identify those full

length clones that showed elevated expression in ethylene induced converter lines relative to ethylene induced converter lines relative to ethylene induced nonconverter burley lines. By so doing, the functionality relationship of full length clones may be determined by comparing biochemical differences in leaf constituents between converter and nonconverter lines. As shown in table below, six clones showed significantly higher expression, as denoted by ++ and +, in converter ethylene treated tissue than that of nonconverter treated tissue, denoted by +. All of these clones showed little or no expression in converter and nonconverter lines that were not ethylene treated.

Full Length Clones	Converter	Nonconverter
D101-BA2	++	+
D207-AA5	++	+
D208-AC8	+++	+
D237-AD1	++	+
D89-AB1	++	+
D90A-BB3	++	+

#### EXAMPLE 8: IMMUNODETECTION OF p450S ENCODED BY THE CLONED GENES

Peptide regions corresponding to 20-22 amino acids in length from three p450 clones were selected for 1) having lower or no homology to other clones and 2) having good hydrophilicity and antigenicity. The amino acid sequences

of the peptide regions selected from the respective p450 clones are listed below. The synthesized peptides were conjugated with KHL and then injected into rabbits. Antisera were collected 2 and 4 weeks after the 4<sup>th</sup> injection (Alpha Diagnostic Intl. Inc. San Antonio, TX).

D234-AD1 DIDGSKSKLVKAHRKIDEILG  
D90a-BB3 RDAFREKETFDENDVEELNY  
D89-AB1 FKNNGDEDRHFSQKLGLADKY

Antisera were examined for crossreactivity to target proteins from tobacco plant tissue by Western Blot analysis. Crude protein extracts were obtained from ethylene treated (0 to 40 hours) middle leaves of converter and nonconverter lines. Protein concentrations of the extracts were determined using RC DC Protein Assay Kit (BIO-RAD) following the manufacturer's protocol.

Two micrograms of protein were loaded onto each lane and the proteins separated on 10% - 20% gradient gels using the Laemmli SDS-PAGE system. The proteins were transferred from gels to PROTRAN® Nitrocellulose Transfer Membranes (Schleicher & Schuell) with the Trans-Blot® Semi-Dry cell (BIO-RAD). Target p450 proteins were detected and visualized with the ECL Advance™ Western Blotting Detection Kit (Amersham Biosciences). Primary antibodies against the synthetic-KLH conjugates were made in rabbits. Secondary antibody against rabbit IgG, coupled with peroxidase, was purchased from Sigma. Both primary and secondary antibodies were used at 1:1000 dilutions. Antibodies showed strong

reactivity to a single band on the Western Blots indicating that the antisera were monospecific to the target peptide of interest. Antisera were also crossreactive with synthetic peptides conjugated to KLH.

5  
EXAMPLE 9: NUCLEIC ACID IDENTITY AND STRUCTURE RELATEDNESS  
OF ISOLATED NUCLEIC ACID FRAGMENTS

10 Over 100 cloned p450 fragments were sequenced in conjunction with Northern blot analysis to determine their structural relatedness. The approach used utilized forward primers based either of two common p450 motifs located near the carboxyl-terminus of the p450 genes. The forward  
15 primers corresponded to cytochrome p450 motifs FXPERF or GRRXCP(A/G) as denoted in Figure 1. The reverse primers used standard primers from either the plasmid, SP6 or T7 located on both arms of pGEM™ plasmid, or a poly A tail. The protocol used is described below.

20 Spectrophotometry was used to estimate the concentration of starting double stranded DNA following the manufacturer's protocol (Beckman Coulter). The template was diluted with water to the appropriate concentration, denatured by heating at 95° C for 2 minutes, and  
25 subsequently placed on ice. The sequencing reaction was prepared on ice using 0.5 to 10µl of denatured DNA template, 2 µl of 1.6 pmole of the forward primer, 8 µl of DTCS Quick Start Master Mix and the total volume brought to 20 µl with water. The thermocycling program consisted of 30 cycles of  
30 the follow cycle: 96° C for 20 seconds, 50° C for 20

seconds, and 60° C for 4 minutes followed by holding at 4° C.

5 The sequence was stopped by adding 5 µl of stop buffer (equal volume of 3M NaOAc and 100mM EDTA and 1 µl of 20 mg/ml glycogen). The sample was precipitated with 60 µl of cold 95% ethanol and centrifuged at 6000g for 6 minutes. Ethanol was discarded. The pellet was 2 washes with 200 µl of cold 70% ethanol. After the pellet was dry, 40 µl of SLS solution was added and the pellet was resuspended. A layer of mineral oil was over laid. The sample was then, placed on the CEQ 8000 Automated Sequencer for further analysis.

15 In order to verify nucleic acid sequences, nucleic acid sequence was re-sequenced in both directions using forward primers to the FXPERF or GRRXCP(A/G) region of the p450 gene or reverse primers to either the plasmid or poly A tail. All sequencing was performed at least twice in both directions.

20 The nucleic acid sequences of cytochrome p450 fragments were compared to each other from the coding region corresponding to the first nucleic acid after the region encoding the GRRXCP(A/G) motif through to the stop codon. This region was selected as an indicator of genetic diversity among p450 proteins. A large number of 25 genetically distinct p450 genes, in excess of 70 genes, were observed, similar to that of other plant species. Upon comparison of nucleic acid sequences, it was found that the genes could be placed into distinct sequences groups based on their sequence identity. It was found that the best 30



unique grouping of p450 members was determined to be those sequences with 75% nucleic acid identity or greater (shown in Table I). Reducing the percentage identity resulted in significantly larger groups. A preferred grouping was observed for those sequences with 81% nucleic acid identity or greater, a more preferred grouping 91% nucleic acid identity or greater, and a most preferred grouping for those sequences 99% nucleic acid identity or greater. Most of the groups contained at least two members and frequently three or more members. Others were not repeatedly discovered suggesting that approach taken was able to isolated both low and high expressing mRNA in the tissue used.

Based on 75% nucleic acid identity or greater, two cytochrome p450 groups were found to contain nucleic acid sequence identity to previously tobacco cytochrome genes that genetically distinct from that within the group. Group 23, showed nucleic acid identity, within the parameters used for Table I, to prior GenBank sequences of GI:1171579 (CAA64635) and GI:14423327 (or AAK62346) by Czernic et al and Ralston et al, respectively. GI:1171579 had nucleic acid identity to Group 23 members ranging 96.9% to 99.5% identity to members of Group 23 while GI:14423327 ranged 95.4% to 96.9% identity to this group. The members of Group 31 had nucleic acid identity ranging from 76.7% to 97.8% identity to the GenBank reported sequence of GI:14423319 (AAK62342) by Ralston et al. None of the other p450 identity groups of Table 1 contained parameter identity, as used in Table 1, to Nicotiana p450s genes reported by

Ralston et al, Czernic et al., Wang et al or LaRosa and Smigocki.

As shown in Figure 76, consensus sequence with  
appropriate nucleic acid degenerate probes could be derived  
for group to preferentially identify and isolate additional  
members of each group from Nicotiana plants.

10

Table I: Nicotiana p450 Nucleic Acid Sequence Identity  
Groups

GROUP      FRAGMENTS

5	1	D58-BG7 (SEQ ID No.:1), D58-AB1 (SEQ ID No.:3); D58-BE4 (SEQ ID No.:7)
	2	D56-AH7 (SEQ ID No.:9); D13a-5 (SEQ ID No.:11)
	3	D56-AG10 (SEQ ID No.:13); D35-33 (SEQ ID No.:15);
10		D34-62 (SEQ ID No.:17)
	4	D56-AA7 (SEQ ID No.:19); D56-AE1 (SEQ ID No.:21);
		185-BD3 (SEQ ID No.:143)
	5	D35-BB7 (SEQ ID No.:23); D177-BA7 (SEQ ID No.:25);
		D56A-AB6 (SEQ ID No.:27); D144-AE2 (SEQ ID No.:29)
15	6	D56-AG11 (SEQ ID No.:31); D179-AA1 (SEQ ID No.:33)
	7	D56-AC7 (SEQ ID No.:35); D144-AD1 (SEQ ID No.:37)
	8	D144-AB5 (SEQ ID No.:39)
	9	D181-AB5 (SEQ ID No.:41); D73-Ac9 (SEQ ID No.:43)
	10	D56-AC12 (SEQ ID No.:45)
20	11	D58-AB9 (SEQ ID No.:47); D56-AG9 (SEQ ID No.:49);
		D56-AG6 (SEQ ID No.:51); D35-BG11 (SEQ ID No.:53); D35-42
		(SEQ ID No.:55); D35-BA3 (SEQ ID No.:57); D34-57 (SEQ ID
		No.:59); D34-52 (SEQ ID No.:61); D34-25 (SEQ ID No.:63)
	12	D56-AD10 (SEQ ID No.:65)
25	13	56-AA11 (SEQ ID No.:67)
	14	D177-BD5 (SEQ ID No.:69); D177-BD7 (SEQ ID No.:83)

15 D56A-AG10 (SEQ ID No.:71); D58-BC5 (SEQ ID No.:73);  
 D58-AD12 (SEQ ID No.:75)  
 16 D56-AC11 (SEQ ID No.:77); D35-39 (SEQ ID No.:79);  
 D58-BH4 (SEQ ID No.:81); D56-AD6 (SEQ ID No.:87)  
 5 17 D73A-AD6 (SEQ ID No.:89); D70A-BA11 (SEQ ID No.:91)  
 18 D70A-AB5 (SEQ ID No.:95); D70A-AA8 (SEQ ID No.:97)  
 19 D70A-AB8 (SEQ ID No.:99); D70A-BH2 (SEQ ID No.:101);  
 D70A-AA4 (SEQ ID No.:103)  
 20 D70A-BA1 (SEQ ID No.:105); D70A-BA9 (SEQ ID No.:107)  
 10 21 D70A-BD4 (SEQ ID No.:109)  
 22 D181-AC5 (SEQ ID No.:111); D144-AH1 (SEQ ID No.:113);  
 D34-65 (SEQ ID No.:115)  
 23 D35-BG2 (SEQ ID No.:117)  
 24 D73A-AH7 (SEQ ID No.:119)  
 15 25 D58-AA1 (SEQ ID No.:121); D185-BC1 (SEQ ID No.:133);  
 D185-BG2 (SEQ ID No.:135)  
 26 D73-AE10 (SEQ ID No.:123)  
 27 D56-AC12 (SEQ ID No.:125)  
 28 D177-BF7 (SEQ ID No.:127); D185-BE1 (SEQ ID No.:137);  
 20 D185-BD2 (SEQ ID No.:139)  
 29 D73A-AG3 (SEQ ID No.:129)  
 30 D70A-AA12 (SEQ ID No.:131); D176-BF2 (SEQ ID No.:85)  
 31 D176-BC3 (SEQ ID No.:145)  
 32 D176-BB3 (SEQ ID No.: 147)

EXAMPLE 10: RELATED AMINO ACID SEQUENCE IDENTITY OF  
ISOLATED NUCLEIC ACID FRAGMENTS

5 The amino acid sequences of nucleic acid sequences  
obtained for cytochrome p450 fragments from Example 8  
were deduced. The deduced region corresponded to the  
amino acid immediately after the GXRXCP(A/G) sequence  
10 motif to the end of the carboxyl-terminus, or stop  
codon. Upon comparison of sequence identity of the  
fragments, a unique grouping was observed for those  
sequences with 70% amino acid identity or greater. A  
preferred grouping was observed for those sequences  
15 with 80% amino acid identity or greater, more preferred  
with 90% amino acid identity or greater, and a most  
preferred grouping for those sequences 99% amino acid  
identity of greater. The groups and corresponding  
amino acid sequences of group members are shown in  
20 Figure 2. Several of the unique nucleic acid sequences  
were found to have complete amino acid identity to  
other fragments and therefore only one member with the  
identical amino acid was reported.

25 The amino acid identity for Group 19 of Table II  
corresponded to three distinct groups based on their  
nucleic acid sequences. The amino acid sequences of  
each group member and their identity is shown in  
Figure. 77. The amino acid differences are  
30 appropriated marked.

At least one member of each amino acid identity group was selected for gene cloning and functional studies using plants. In addition, group members that are differentially affected by ethylene treatment or other biological differences as assessed by Northern and Southern analysis were selected for gene cloning and functional studies. To assist in gene cloning, expression studies and whole plant evaluations, peptide specific antibodies will be prepared on sequence identity and differential sequence.

Table II: Nicotiana p450 Amino Acid Sequence Identity Groups

GROUP            FRAGMENTS

5	1	D58-BG7 (SEQ ID No.:2), D58-AB1 (SEQ ID No.:4)
	2	D58-BE4 (SEQ ID No.:8)
	3	D56-AH7 (SEQ ID No.:10); D13a-5 (SEQ ID No.:12)
	4	D56-AG10 (SEQ ID
10		No.:14); D34-62 (SEQ ID No.:18)
	5	D56-AA7 (SEQ ID No.:20); D56-AE1 (SEQ ID No.:22); 185-
		BD3 (SEQ ID No.:144)
	6	D35-BB7 (SEQ ID No.:24); D177-BA7 (SEQ ID No.:26);
		D56A-AB6 (SEQ ID No.:28); D144-AE2 (SEQ ID No.:30)
15	7	D56-AG11 (SEQ ID No.:32); D179-AA1 (SEQ ID No.:34)
	8	D56-AC7 (SEQ ID No.:36); D144-AD1 (SEQ ID No.:38)
	9	D144-AB5 (SEQ ID No.:40)
	10	D181-AB5 (SEQ ID No.:42); D73-Ac9 (SEQ ID No.:44)
	11	D56-AC12 (SEQ ID No.:46)
20	12	D58-AB9 (SEQ ID No.:48); D56-AG9 (SEQ ID No.:50); D56-
		AG6 (SEQ ID No.:52); D35-BG11 (SEQ ID No.:54); D35-42 (SEQ
		ID No.:56); D35-BA3 (SEQ ID No.:58); D34-57 (SEQ ID
		No.:60); D34-52 (SEQ ID No.:62)
	13	D56AD10 (SEQ ID No.:66)
25	14	56-AA11 (SEQ ID No.:68)
	15	D177-BD5 (SEQ ID No.:70); D177-BD7 (SEQ ID No.:84)

16 D56A-AG10 (SEQ ID No.:72); D58-BC5 (SEQ ID No.:74);  
 D58-AD12 (SEQ ID No.:76)  
 17 D56-AC11 (SEQ ID No.:78); D56-AD6 (SEQ ID No.:88)  
 18 D73A-AD6 (SEQ ID No.90:)  
 5 19 D70A-AB5 (SEQ ID No.:96); D70A-AB8 (SEQ ID No.:100);  
 D70A-BH2 (SEQ ID No.:102); D70A-AA4 (SEQ ID No.:104); D70A-  
 BA1 (SEQ ID No.:106); D70A-BA9 (SEQ ID No.:108)  
 20 D70A-BD4 (SEQ ID No.:110)  
 21 D181-AC5 (SEQ ID No.:112); D144-AH1 (SEQ ID No.:114);  
 10 D34-65 (SEQ ID No.:116)  
 22 D35-BG2 (SEQ ID No.:118)  
 23 D73A-AH7 (SEQ ID No.:120)  
 24 D58-AA1 (SEQ ID No.:122); D185-BC1 (SEQ ID No.:134);  
 D185-BG2 (SEQ ID No.:136)  
 15 25 D73-AE10 (SEQ ID No.:124)  
 26 D56-AC12 (SEQ ID No.:126)  
 27 D177-BF7 (SEQ ID No.:128); 185-BD2 (SEQ ID No.:140)  
 28 D73A-AG3 (SEQ ID No.:130)  
 29 D70A-AA12 (SEQ ID No.:132); D176-BF2 (SEQ ID No.:86)  
 20 30 D176-BC3 (SEQ ID No.:146)  
 31 D176-BB3 (SEQ ID No.:148)  
 32 D186-AH4 (SEQ ID No.:6)



EXAMPLE 11: RELATED AMINO ACID SEQUENCE IDENTITY OF FULL LENGTH CLONES

The nucleic acid sequence of full length Nicotiana genes cloned in Example 5 were deduced for their entire amino acid sequence. Cytochrome p450 genes were identified by the presence of three conserved p450 domain motifs, which corresponded to UXXRXXZ, PXRFXF or GXRXC at the carboxyl-terminus where U is E or K, X is any amino acid and Z is P, T, S or M. It was also noted that two of the clones appeared nearly complete but lacked the appropriate stop codon, D130-AA1 and D101-BA2, however but both contained all three p450 cytochrome domains. All p450 genes were characterized for amino acid identity using a BLAST program comparing their full length sequences to each other and to known tobacco genes. The program used the NCBI special BLAST tool (Align two sequences (b12seq), <http://www.ncbi.nlm.nih.gov/blast/b12seq/b12.html>). Two sequences were aligned under BLASTN without filter for nucleic acid sequences and BLASTP for amino acid sequences. Based on their percentage amino acid identity, each sequence was grouped into identity groups where the grouping contained members that shared at least 85% identity with another member. A preferred grouping was observed for those sequences with 90% amino acid identity or greater, a more preferred grouping had 95% amino acid identity or greater, and a most preferred grouping had those sequences 99% amino acid identity or greater. Using these criteria, 25 unique groups were identified and are depicted in Table III.

Within the parameters used for Table III for amino acid identity, three groups were found to contain greater than 85% or greater identity to known tobacco genes. Members of Group 5 had up to 96% amino acid identity for full length sequences to prior GenBank sequences of GI:14423327 (or AAK62346) by Ralston et al. Group 23 had up to 93% amino acid identity to GI:14423328 (or AAK62347) by Ralston et al. and Group 24 had 92% identity to GI:14423318 (or AAK62343) by Ralston et al.

Table III: Amino Acid Sequence Identity Groups of Full Length Nicotiana p450 Genes

- 1 D208-AD9 (SEQ. ID. No. 224); D120-AH4 (SEQ. ID. No. 180); D121-AA8 (SEQ. ID. No. 182), D122-AF10 (SEQ. ID. No. 184); D103-AH3 (SEQ. ID. No. 222); D208-AC8 (SEQ. ID. No. 218); D-235-ABI (SEQ. ID. No. 246)
- 2 D244-AD4 (SEQ. ID. No. 250); D244-AB6 (SEQ. ID. No. 274) ; D285-AA8; D285-AB9; D268-AE2 (SEQ. ID. No. 270)
- 3 D100A-AC3 (SEQ. ID. No. 168); D100A-BE2
- 4 D205-BE9 (SEQ. ID. No. 276); D205-BG9 (SEQ. ID. No. 202); D205-AH4 (SEQ. ID. No. 294)
- 5 D259-AB9 (SEQ. ID. No. 260) ; D257-AE4 (SEQ. ID. No. 268); D147-AD3 (SEQ. ID. No. 194)
- 6 D249-AE8 (SEQ. ID. No. 256); D-248-AA6 (SEQ. ID. No. 254)
- 7 D233-AG7 (SEQ. ID. No. 266; D224-BD11 (SEQ. ID. No. 240); DAF10
- 8 D105-AD6 (SEQ. ID. No. 172); D215-AB5 (SEQ. ID. No. 220); D135-AE1 (SEQ. ID. No. 190)

9 D87A-AF3 (SEQ. ID. No. 216), D210-BD4 (SEQ. ID. No.  
 262)  
 10 D89-AB1 (SEQ. ID. No. 150); D89-AD2 (SEQ. ID. No. 152);  
 163-AG11 (SEQ. ID. No. 198); 163-AF12 (SEQ. ID. No.  
 196)  
 11 D267-AF10 (SEQ. ID. No. 296); D96-AC2 (SEQ. ID. No.  
 160); D96-AB6 (SEQ. ID. No. 158); D207-AA5 (SEQ. ID.  
 No. 204); D207-AB4 (SEQ. ID. No. 206); D207-AC4 (SEQ.  
 ID. No. 208)  
 12 D98-AG1 (SEQ. ID. No. 164); D98-AA1 (SEQ. ID. No. 162)  
 13 D209-AA12 (SEQ. ID. No. 212); D209-AA11; D209-AH10  
 (SEQ. ID. No. 214); D209-AH12 (SEQ. ID. No. 232);  
 D90a-BB3 (SEQ. ID. No. 154)  
 14 D129-AD10 (SEQ. ID. No. 188); D104A-AE8 (SEQ. ID. No.  
 170)  
 15 D228-AH8 (SEQ. ID. No. 244); D228-AD7 (SEQ. ID. No.  
 241), D250-AC11 (SEQ. ID. No. 258); D247-AH1 (SEQ.  
 ID. No. 252)  
 16 D128-AB7 (SEQ. ID. No. 186) ; D243-AA2 (SEQ. ID. No.  
 248); D125-AF11 (SEQ. ID. No. 228)  
 17 D284-AH5 (SEQ. ID. No. 298); D110-AF12 (SEQ. ID. No.  
 176)  
 18 D221-BB8 (SEQ. ID. No. 234)  
 19 D222-BH4 (SEQ. ID. No. 236)  
 20 D134-AE11 (SEQ. ID. No. 230)  
 21 D109-AH8 (SEQ. ID. No. 174)  
 22 D136-AF4 (SEQ. ID. No. 278)  
 23 D237-AD1 (SEQ. ID. No. 226)  
 24 D112-AA5 (SEQ. ID. No. 178)  
 25 D283-AC1 (SEQ. ID. No. 272)

The full length genes were further grouped based on the highly conserved amino acid homology between UXXRXXZ p450 domain and GXRXC p450 domain near the end the carboxyl-terminus. As shown in Figure 3, individual clones were aligned for their sequence homology between the conserved domains relative to each other and placed in distinct identity groups. In several cases, although the nucleic acid sequence of the clone was unique, the amino acid sequence for the region was identical. The preferred grouping was observed for those sequences with 90% amino acid identity or greater, a more preferred group had 95% amino acid identity or greater, and a most preferred grouping had those sequences 99% amino acid identity or greater. The final grouping was similar to that based on the percent identity for the entire amino acid sequence of the clones except for Group 17 (of Table III) which was divided into two distinct groups.

Within the parameters used for amino acid identity in Table IV, three groups were found to contain 90% or greater identity to known tobacco genes. Members of Group 5 had up to 93.4% amino acid identity for full length sequences to prior GenBank sequences of GI:14423326 (AAK62346) by Ralston et al. Group 23 had up to 91.8% amino acid identity to GI:14423328 (or AAK62347) by Ralston et al. and Group 24 had 98.8% identity to GI:14423318 (or AAK62342) by Ralston et al.

Table IV: Amino Acid Sequence Identity Groups of Regions between Conserved Domains of Nicotiana p450 Genes

1 1 D208-AD9 (SEQ. ID. No. 224); D120-AH4 (SEQ. ID. No.  
 180); D121-AA8 (SEQ. ID. No. 182), D122-AF10 (SEQ. ID.  
 No. 184); D103-AH3 (SEQ. ID. No. 222); D208-AC8 (SEQ.  
 ID. No. 218); D-235-ABI (SEQ. ID. No. 246)  
 2 D244-AD4 (SEQ. ID. No. 250); D244-AB6 (SEQ. ID. No.  
 274) ; D285-AA8; D285-AB9; D268-AE2 (SEQ. ID. No. 270)  
 3 D100A-AC3 (SEQ. ID. No. 168); D100A-BE2  
 4 D205-BE9 (SEQ. ID. No. 276); D205-BG9 (SEQ. ID. No.  
 202); D205-AH4 (SEQ. ID. No. 294)  
 10 5 D259-AB9 (SEQ. ID. No. 260) ; D257-AE4 (SEQ. ID. No.  
 268); D147-AD3 (SEQ. ID. No. 194)  
 6 D249-AE8 (SEQ. ID. No. 256); D-248-AA6 (SEQ. ID. No.  
 254)  
 7 D233-AG7 (SEQ. ID. No. 266; D224-BD11 (SEQ. ID. No.  
 15 240); DAF10  
 8 D105-AD6 (SEQ. ID. No. 172); D215-AB5 (SEQ. ID. No.  
 220); D135-AE1 (SEQ. ID. No. 190)  
 9 D87A-AF3 (SEQ. ID. No. 216), D210-BD4 (SEQ. ID. No.  
 262)  
 20 10 D89-AB1 (SEQ. ID. No. 150); D89-AD2 (SEQ. ID. No. 152);  
 163-AG11 (SEQ. ID. No. 198); 163-AF12 (SEQ. ID. No.  
 196)  
 11 D267-AF10 (SEQ. ID. No. 296); D96-AC2 (SEQ. ID. No.  
 160); D96-AB6 (SEQ. ID. No. 158); D207-AA5 (SEQ. ID.  
 25 No. 204); D207-AB4 (SEQ. ID. No. 206); D207-AC4 (SEQ.  
 ID. No. 208)  
 12 D98-AG1 (SEQ. ID. No. 164); D98-AA1 (SEQ. ID. No. 162)  
 13 D209-AA12 (SEQ. ID. No. 212); D209-AA11; D209-AH10  
 (SEQ. ID. No. 214); D209-AH12 (SEQ. ID. No. 232);  
 30 D90a-BB3 (SEQ. ID. No. 154)

- 14 D129-AD10 (SEQ. ID. No. 188); D104A-AE8 (SEQ. ID. No. 170)
- 15 D228-AH8 (SEQ. ID. No. 244); D228-AD7 (SEQ. ID. No. 241), D250-AC11 (SEQ. ID. No. 258); D247-AH1 (SEQ. ID. No. 252)
- 16 D128-AB7 (SEQ. ID. No. 186) ; D243-AA2 (SEQ. ID. No. 248); D125-AF11 (SEQ. ID. No. 228)
- 17 D284-AH5 (SEQ. ID. No. 298); D110-AF12 (SEQ. ID. No. 176)
- 18 D221-BB8 (SEQ. ID. No. 234)
- 19 D222-BH4 (SEQ. ID. No. 236)
- 20 D134-AE11 (SEQ. ID. No. 230)
- 21 D109-AH8 (SEQ. ID. No. 174)
- 22 D136-AF4 (SEQ. ID. No. 278)
- 23 D237-AD1 (SEQ. ID. No. 226)
- 24 D112-AA5 (SEQ. ID. No. 178)
- 25 D283-AC1 (SEQ. ID. No. 272)
- 26 D110-AF12 (SEQ. ID. No. 176)

EXAMPLE 12: NICOTIANA CYTOCHROME P450 CLONES LACKING ONE OR MORE OF THE TOBACCO CYTOCHROME P450 SPECIFIC DOMAINS

Four clones had high nucleic acid homology, ranging 90% to 99% nucleic acid homology, to other tobacco cytochrome genes reported in Table III. The four clones included D136-AD5, D138-AD12, D243-AB3 and D250-AC11. However, due to a nucleotide frameshift these genes did not contain one or more of three C-terminus cytochrome p450 domains and were excluded from identity groups presented in Table III or Table IV.

The amino acid identity of one clone, D95-AG1, did not contain the third domain, GXRXC, used to group p450 tobacco genes in Table III or Table IV. The nucleic acid homology of this clone had low homology to other tobacco cytochrome genes. This clone represents a novel and different group of cytochrome p450 genes in Nicotiana.

EXAMPLE 13: USE OF NICOTIANA CYTOCHROME P450 FRAGMENTS AND CLONES IN ALTERED REGULATION OF TOBACCO PROPERTIES

The use of tobacco p450 nucleic acid fragments or whole genes are useful in identifying and selecting those plants that have altered tobacco phenotypes or tobacco constituents and, more importantly, altered metabolites. Transgenic tobacco plants are generated by a variety of transformation systems that incorporate nucleic acid fragments or full length genes, selected from those reported herein, in orientations for either down-regulation, for example anti-sense orientation, or over-expression for example, sense orientation. For over-expression to full length genes, any nucleic acid sequence that encodes the entire or a functional part or amino acid sequence of the full-length genes described in this invention are desired that are effective for increasing the expression of a certain enzyme and thus resulting in phenotypic effect within Nicotiana. Nicotiana lines that are homozygous lines are obtained through a series of backcrossing and assessed for phenotypic changes including, but not limited to, analysis of endogenous p450 RNA, transcripts, p450 expressed peptides and concentrations of plant metabolites using techniques commonly available to one having ordinary skill in the art.

The changes exhibited in the tobacco plants provide information on the functional role of the selected gene of interest or are of a utility as a preferred Nicotiana plant species.

5 Numerous modifications and variations in practice of the invention are expected to occur to those skilled in the art upon consideration of the foregoing detailed description of the invention. Consequently, such modifications and  
10 variations are intended to be included within the scope of the following claims.